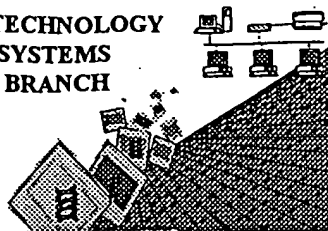


Link

RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY
SYSTEMS
BRANCH



The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/537,710
Source: 1600
Date Processed by STIC: 4/8/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/efb/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name,
Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two,
2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office,
Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

Raw Sequence Listing Error Summary

1600

ERROR DETECTED

SUGGESTED CORRECTION

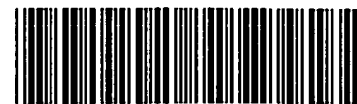
SERIAL NUMBER: 09/537,710

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 Wrapped Nucleics
 Wrapped Aminos The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 Invalid Line Length The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 Misaligned Amino
 Numbering The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 Non-ASCII The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 Variable Length Sequence(s) contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 PatentIn 2.0
 "bug" A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 Skipped Sequences
 (OLD RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence:
 (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
 (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
 This sequence is intentionally skipped

 Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 Skipped Sequences
 (NEW RULES) Sequence(s) missing. If intentional, please insert the following lines for each skipped sequence.
 <210> sequence id number
 <400> sequence id number
 000
- 9 ✓ Use of n's or Xaa's
 (NEW RULES) Use of n's and/or Xaa's have been detected in the Sequence Listing.
 Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
 In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 Invalid <213>
 Response Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 Use of <220> Sequence(s) missing the <220> "Feature" and associated numeric identifiers and responses.
 Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
 (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 PatentIn 2.0
 "bug" Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 Misuse of n n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

BEST AVAILABLE COPY



Does Not Comply
Corrected Diskette Needed

1600

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/537,710

DATE: 04/08/2002
TIME: 10:57:03

Input Set : A:\EP.txt
Output Set: N:\CRF3\04082002\I537710.raw

3 <110> APPLICANT: Dahlqvist, Andres
4 Stahl, Ulf
5 Lenman, Marit
6 Banas, Antoni
7 Ronne, Hans
9 <120> TITLE OF INVENTION: A new class of enzymes in the biosynthetic pathway for the
production
10 of
11 triacylglycerol and recombinant DNA molecules encoding these enzymes
13 <130> FILE REFERENCE: BASFnae337799PCT1-15
15 <140> CURRENT APPLICATION NUMBER: US 09/537,710
17 <141> CURRENT FILING DATE: 2000-03-30
19 <150> PRIOR APPLICATION NUMBER: EP 99106656.4
20 <151> PRIOR FILING DATE: 1999-04-01
22 <160> NUMBER OF SEQ ID NOS: 31
24 <170> SOFTWARE: WordPerfect version 6.1

ERRORED SEQUENCES

457 <210> SEQ ID NO: 5
458 <211> LENGTH: 2427
459 <212> TYPE: DNA
460 <213> ORGANISM: Arabidopsis thaliana
462 <400> SEQUENCE: 5
463 agaaacagct ctttgtctct ctcgactgat ctaacaatcc ctaatctgtg ttctaaattc 60
464 ctggacgaga ttgacaaaag tccgtatagc ttaacctggt ttaatttcaa gtgacagata 120
465 tgcccttat tcatcggaaa aagccgacgg agaaaccatc gacgcccga tctgaagagg 180
466 tgggtgcacga tgaggattcg caaaagaaac cacacgaatc ttccaaatcc caccataaga 240
467 aatcgaacgg aggagggaag tggctgtgca tcgattcttg ttggttggtc attgggtgtg 300
468 tgtgtgtaac ctggtggttt cttctcttcc tttaacaacg aatgcctgcg agcttccctc 360
469 agtatgtaac ggagcgaatc acgggtcctt tgccctgaacc gcccggtggt aagctcaaaa 420
470 aaagaagggtc ttaaggcgaa acatcctggt gtcttcattc ctgggattgt caccggtggg 480
471 ctcgagcttt gggaaggcaa acaatgcgct gatggtttat ttagaaaacg tttgtggggt 540
472 ggaacttttg gtgaagtcta caaaaggcct ctatgttggg tggaacacat gtcacttgac 600
473 aatgaaactg ggttggatcc agctggtatt agagttcgag ctgtatcagg actcgtggct 660
474 gctgactact ttgctcctgg ctactttgtc tgggcagtgc tgattgctaa ccttgacat 720
475 attggatatg aagagaaaaa tatgtacatg gctgcatatg actggcggct ttcgtttcag 780
476 aacacagagg tacgtgatca gactcttagc cgtatgaaaa gtaatataga gttgatggtt 840
477 tctaccaacg gtggaaaaaa agcagttata gttccgcatt ccatgggggt cttgtatttt 900
478 ctacatttta tgaagtgggt tgaggcacca gtcctctggt gtggcggggg tgggccagat 960
479 tgggtgtgaa agtatattaa ggcgggtgat aacattgggt gaccatttct tgggtgttcca 1020
480 aaagctgttg cagggtttt ctctgctgaa gcaaaggatg ttgcagttgc cagagcgatt 1080
481 gccccaggat tcttagacac cgatatattt agacttcaga ccttgcagca tgtaatgaga 1140

The type of errors shown exist throughout
the Sequence Listing. Please check subsequent
sequences for similar errors.

*Ns detected in sequence -
requires explanation; see error
summary sheet item 9*

RAW SEQUENCE LISTING

DATE: 04/08/2002

PATENT APPLICATION: US/09/537,710

TIME: 10:57:03

Input Set : A:\EP.txt

Output Set: N:\CRF3\04082002\I537710.raw

```

482 atgacacgca catgggactc aacaatgtct atgttaccga agggagggtga caccgatatgg 1200
483 ggcgggcttg attggtcacc ggagaaaggc cacacctgtt gtgggaaaaa gcaaaagaac 1260
484 aacgaaactt gtggtgaagc aggtgaaaac ggagtttcca agaaaagtcc tgttaactat 1320
485 ggaaggatga tatcttttgg gaaagaagta gcagaggctg cgccatctga gattaataat 1380
486 attgattttc gaggtgctgt caaaggtcag agtatcccaa atcacacctg tcgtgacgtg 1440
487 tggacagagt accatgacat ggggaattgct gggatcaaag ctatcgctga gtataaggtc 1500
488 tacactgctg gtgaagctat agatctacta cattatgttg ctctaagat gatggcgctg 1560
489 ggtgccgctc atttctctta tgggaattgct gatgatttgg atgacaccaa gtatcaagat 1620
490 cccaaatact ggtcaaatacc gttagagaca aaattaccga atgctcctga gatggaaatc 1680
491 tactcattat acggagtggtg gataccaacg gaacgagcat acgtatacaa gcttaaccag 1740
492 tctcccgaca gttgcatccc ctttcagata ttcacttctg ctcacgagga ggacgaagat 1800
493 agctgtctga aagcaggagt ttacaatgtg gatggggatg aaacagtacc cgtcctaagt 1860
494 gccgggtaca tgtgtgcaaa agcgtggcgt ggcaagacaa gattcaaccc ttccggaatc 1920
495 aagacttata taagagaata caatcactct ccgccggcta acctgttggg agggcgcggtg 1980
496 acgcagagtg gtgcccattg tgatatcatg ggaaactttg ctttgatcga agatatcatg 2040
497 agggttgccg ccggaggtaa cgggtctgat ataggacatg accagggtcca ctctggcata 2100
498 tttgaatggt cggagcgtat tgacctgaag ctgtgaatat catgatctct ttaagctgtc 2160
499 ctgtcagctt atgtgaatcc aatactttga aagagagatc atcatcaatt catcatcatc 2220
500 gtcatcatca tgatgtctaa ctacaaaaga agcctgagaa tgatactttg gtgcgaaatt 2280
501 ctcaatacct ctttaatat tttattgaat gttaaattata caatcctatc taatgtttga 2340
E--> 502 acgataacac aaaacttgct gggccatgt ttgtttgtct tgtcaaaagc atcaatttgt 2400
503 gggttaaaaa aaaaaaaaaa aaaaaaa 2427
719 <210> SEQ ID NO: 9
720 <211> LENGTH: 616
721 <212> TYPE: DNA
722 <213> ORGANISM: Neurospora crassa
724 <400> SEQUENCE: 9
E--> 725 ggtggcgaag acgagggcgg aagttggagg ctaacgagaa tgacnctcgg agatggatct 60
E--> 726 accctctaga gacacgacta cctttgcacc cagcctcaag gntacngtt tntatgggta 120
727 ggaagccgac ggagcgcagc tacatctatc tggcgccgca tcccgggacg acaacgcac 180
E--> 728 tttagatgac gatcgatacg actttgactn aggggcacat tgaccacggg gtgattttgg 240
729 gcgaaggcga tggcacagtg aaccttatga gtttggggta cctgtgcaat aaggggtgga 300
730 aatgaagag atacaatcct gcgggctcaa aaataaccgt ggtcgagatg ccgcataaac 360
731 cagaacggtt caatccgaga ggagggccga atacggcgga tcacgtggat attctaggaa 420
732 ggcagaatct aaacgagtag attcttaaag tggcggcagg tcgaggcgat acaattgagg 480
733 attttattac tagtaatat cttaaatatg tagaaaaggt tgaaatttat gaagagtaat 540
734 taaatacggc acataggtta ctcaatagta tgactaatta aaaaaaaatt ttttttctaa 600
735 aaaaaaaaaa aaaaaa 616
866 <210> SEQ ID NO: 13
867 <211> LENGTH: 623
868 <212> TYPE: PRT
869 <213> ORGANISM: Schizosaccharomyces pombe
E--> 871 <400> SEQUENCE: 15
872 Met Ala Ser Ser Lys Lys Ser Lys Thr His Lys Lys Lys Lys Glu Val
873 1 5 10 15
875 Lys Ser Pro Ile Asp Leu Pro Asn Ser Lys Lys Pro Thr Arg Ala Leu
876 20 25 30
878 Ser Glu Gln Pro Ser Ala Ser Glu Thr Gln Ser Val Ser Asn Lys Ser
879 35 40 45

```

Same error

Seq. ID nos differ!

RAW SEQUENCE LISTING

DATE: 04/08/2002

PATENT APPLICATION: US/09/537,710

TIME: 10:57:03

Input Set : A:\EP.txt

Output Set: N:\CRF3\04082002\I537710.raw

```

881 Arg Lys Ser Lys Phe Gly Lys Arg Leu Asn Phe Ile Leu Gly Ala Ile
882      50      55      60
884 Leu Gly Ile Cys Gly Ala Phe Phe Phe Ala Val Gly Asp Asp Asn Ala
885 65      70      75      80
887 Val Phe Asp Pro Ala Thr Leu Asp Lys Phe Gly Asn Met Leu Gly Ser
888      85      90      95
890 Ser Asp Leu Phe Asp Asp Ile Lys Gly Tyr Leu Ser Tyr Asn Val Phe
891      100     105     110
893 Lys Asp Ala Pro Phe Thr Thr Asp Lys Pro Ser Gln Ser Pro Ser Gly
894      115     120     125
896 Asn Glu Val Gln Val Gly Leu Asp Met Tyr Asn Glu Gly Tyr Arg Ser
897      130     135     140
899 Asp His Pro Val Ile Met Val Pro Gly Val Ile Ser Ser Gly Leu Glu
900 145     150     155     160
902 Ser Trp Ser Phe Asn Asn Cys Ser Ile Pro Tyr Phe Arg Lys Arg Leu
903      165     170     175
905 Trp Gly Ser Trp Ser Met Leu Lys Ala Met Phe Leu Asp Lys Gln Cys
906      180     185     190
908 Trp Leu Glu His Leu Met Leu Asp Lys Lys Thr Gly Leu Asp Pro Lys
909      195     200     205
911 Gly Ile Lys Leu Arg Ala Ala Gln Gly Phe Glu Ala Ala Asp Phe Phe
912      210     215     220
914 Ile Thr Gly Tyr Trp Ile Trp Ser Lys Val Ile Glu Asn Leu Ala Ala
915 225     230     235     240
917 Ile Gly Tyr Glu Pro Asn Asn Met Leu Ser Ala Ser Tyr Asp Trp Arg
918      245     250     255
920 Leu Ser Tyr Ala Asn Leu Glu Glu Arg Asp Lys Tyr Phe Ser Lys Leu
921      260     265     270
923 Lys Met Phe Ile Glu Tyr Ser Asn Ile Val His Lys Lys Lys Val Val
924      275     280     285
926 Leu Ile Ser His Ser Met Gly Ser Gln Val Thr Tyr Tyr Phe Phe Lys
927      290     295     300
929 Trp Val Glu Ala Glu Gly Tyr Gly Asn Gly Gly Pro Thr Trp Val Asn
930 305     310     315     320
932 Asp His Ile Glu Ala Phe Ile Asn Ile Ser Gly Ser Leu Ile Gly Ala
933      325     330     335
935 Pro Lys Thr Val Ala Ala Leu Leu Ser Gly Glu Met Lys Asp Thr Gly
936      340     345     350
938 Ile Val Ile Thr Leu Asn Ile Leu Glu Lys Phe Phe Ser Arg Ser Glu
939      355     360     365
941 Arg Ala Met Met Val Arg Thr Met Gly Gly Val Ser Ser Met Leu Pro
942      370     375     380
944 Lys Gly Gly Asp Val Ala Pro Asp Asp Leu Asn Gln Thr Asn Phe Ser
945 385     390     395     400
947 Asn Gly Ala Ile Ile Arg Tyr Arg Glu Asp Ile Asp Lys Asp His Asp
948      405     410     415
950 Glu Phe Asp Ile Asp Asp Ala Leu Gln Phe Leu Lys Asn Val Thr Asp
951      420     425     430
953 Asp Asp Phe Lys Val Met Leu Ala Lys Asn Tyr Ser His Gly Leu Ala

```

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/537,710

DATE: 04/08/2002

TIME: 10:57:03

Input Set : A:\EP.txt

Output Set: N:\CRF3\04082002\I537710.raw

```

954          435          440          445
956 Trp Thr Glu Lys Glu Val Leu Lys Asn Asn Glu Met Pro Ser Lys Trp
957          450          455          460
959 Ile Asn Pro Leu Glu Thr Ser Leu Pro Tyr Ala Pro Asp Met Lys Ile
960 465          470          475          480
962 Tyr Cys Val His Gly Val Gly Lys Pro Thr Glu Arg Gly Tyr Tyr Tyr
963          485          490          495
965 Thr Asn Asn Pro Glu Gly Gln Pro Val Ile Asp Ser Ser Val Asn Asp
966          500          505          510
968 Gly Thr Lys Val Glu Asn Gly Ile Val Met Asp Asp Gly Asp Gly Thr
969          515          520          525
971 Leu Pro Ile Leu Ala Leu Gly Leu Val Cys Asn Lys Val Trp Gln Thr
972          530          535          540
974 Lys Arg Phe Asn Pro Ala Asn Thr Ser Ile Thr Asn Tyr Glu Ile Lys
975 545          550          555          560
977 His Glu Pro Ala Ala Phe Asp Leu Arg Gly Gly Pro Arg Ser Ala Glu
978          565          570          575
980 His Val Asp Ile Leu Gly His Ser Glu Leu Asn Glu Ile Ile Leu Lys
981          580          585          590
983 Val Ser Ser Gly His Gly Asp Ser Val Pro Asn Arg Tyr Ile Ser Asp
984          595          600          605
986 Ile Gln Glu Ile Ile Asn Glu Ile Asn Leu Asp Lys Pro Arg Asn
987          610          615          620

```

2353 <210> SEQ ID NO: 8b

2354 <211> LENGTH: 516

2355 <212> TYPE: DNA

2356 <213> ORGANISM: Neurospora crassa

2358 <400> SEQUENCE: 8b

Some error N's detected

```

E--> 2359 ggtggcgaag acgagggcgg aagttggagg ctaacgagaa tgacnctcgg agatggatct 60
E--> 2360 accctctaga gacacgacta cdnttgacc cagcctcaag gntacngtt thtatgggta 120
2361 ggaagccgac ggagcgagcc tacatctatc tggcgcccga tcccgggacg acaacgcac 180
E--> 2362 tttagatgac gatcgatacg actttgactn aggggcacat tgaccacggt gtgattttgg 240
2363 gcgaaggcga tggcacagtg aacottatga gtttggggta cctgtgcaat aaggggtgga 300
2364 aaatgaagag atacaatcct gcgggctcaa aaataaccgt ggtcgagatg ccgcatgaac 360
2365 cagaacggtt caatccgaga ggagggccga atacggcgga cttaaataatg tagaaaaggt 420
2366 tgaaatttat gaagagtaat taaatacggc acataggtta ctcaatagta tgactaatta 480
2367 aaaaaaattt ttttttctaa aaaaaaaaaa aaaaaa 516

```

VERIFICATION SUMMARY

DATE: 04/08/2002

PATENT APPLICATION: US/09/537,710

TIME: 10:57:04

Input Set : A:\EP.txt

Output Set: N:\CRF3\04082002\I537710.raw

L:502 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5
L:679 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:683 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:7
L:689 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:691 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:7
L:691 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:725 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:9
M:340 Repeated in SeqNo=9
L:871 M:212 E: (34) Invalid or duplicate Sequence ID Number, SEQUENCE ID NOS:13 differs:15
L:2254 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:2254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:2255 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:2255 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:2266 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:2266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:2267 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:5
L:2267 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5
L:2313 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:2317 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:6
L:2323 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:2323 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:2325 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:6
L:2325 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6
L:2359 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:8
M:340 Repeated in SeqNo=8